What is claimed is:

1. A method for extracting intact cytoplasmic biomolecules from cells, which method comprises:
    a. obtaining a fluid sample from a test subject, said fluid sample comprising a mixture of cell populations suspected of containing target cells;
    b. releasing said cytoplasmic biomolecules from said cells;
    c. isolating said cytoplasmic biomolecules; and
    d. analyzing said cytoplasmic biomolecules.
2. The method as claimed in claim 1, wherein said fluid sample is whole blood.
3. The method as claimed in claim 1, wherein selection of said target cells is accomplished by a selecting method from the group consisting of immunomagnetic selection, cell fractionation, and combinations thereof.
4. The method according to claim 1, wherein said releasing step is accomplished by addition of a permeabilizing agent.
5. The method according to claim 4, wherein said permeabilizing agent is selected from the group consisting of a detergent, surfactant, and combinations thereof.
6. The method according to claim 4, wherein said permeabilizing agent is selected from the group consisting of saponin, Immuniperm, and combinations thereof.
7. The method according to claim 4, wherein said permeabilizing agent is Immuniperm.
8. The method according to claim 1, wherein said obtaining said fluid sample includes treating the sample with a cell stabilizing agent.
9. The method according to claim 8, wherein said stabilizing agent is selected from the group consisting of aldehydes, urea, and combinations thereof.
10. The method according to claim 9, wherein said aldehyde is selected from the group consisting of formaldehyde, paraformaldehyde, and combinations thereof.
11. The method according to claim 8, wherein said stabilizing agent is a dialdehyde.
12. The method according to claim 11, wherein said dialdehyde is selected from the group consisting of glutaraldehyde, glyoxal, and combinations thereof.
13. The method according to claim 8, wherein said releasing of said cytoplasmic biomolecules involves macromolecular complexes formed after exposure to said stabilizing agent.

14. The method according to claim 13, wherein said releasing said cytoplasmic biomolecules from said cells is accomplished with enzymatic digestion.
15. The method according to claim 14, wherein said enzymatic digestion is accomplished with a selection from the group of proteinases, nucleophiles, and combinations thereof.
16. The method according to claim 15, wherein said proteinases are selected from the group consisting of proteinase K digestion, V8 proteinase digestion, pronase digestion, and combinations thereof.
17. The method according to claim 15, wherein said nucleophiles are from a group consisting of phosphate-based buffers, tris-based buffers, acetic hydrazide, hydroxylamine, and combinations thereof.
18. The method according to claim 1, wherein said cytoplasmic biomolecules are proteins.
19. The method according to claim 18, wherein said isolating said proteins is accomplished by a method selected from the group consisting of chemical extractions, electrophoresis, chromatography, immunoseparations and affinity techniques.
20. The method according to claim 1, wherein said cytoplasmic biomolecules are nucleic acids.
21. The method according to claim 20, wherein said nucleic acids are selected from the group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.
22. The method according to claim 20, wherein said nucleic acids are cytoplasmic mRNA.
23. The method according to claim 20, wherein the method of isolating said nucleic acids is selected from the group consisting of RNA or DNA chemical extractions, electrophoresis, chromatography, immunoseparations and affinity techniques.
24. The method according to claim 20, wherein said isolating of said nucleic acids is accomplished by capture with magnetic beads affixed to oligo(dT).
25. The method according to claim 1, wherein said target cells are assessed for phenotypic expression other than with said cytoplasmic biomolecules after obtaining said fluid sample.
26. The method according to claim 25, wherein said phenotypic expression is selected from the group consisting of morphological examining, cell component staining, immunoanalyzing, and combinations thereof.

27. The method according to claim 1, wherein said analysis of said cytoplasmic biomolecules is accomplished by functional proteomics.
28. The method according to claim 27, wherein said functional proteomics is selected from the group consisting of protein expression profile, Western blot, amino acid sequence analysis, electrophoresis, 2-D electrophoresis, mass spectrometry, gas chromatography, liquid chromatography nuclear magnetic resonance, infrared, atomic adsorption, and combinations thereof.
29. The method according to claim 1, wherein said analyzing of said cytoplasmic biomolecules is accomplished by functional genomics.
30. The method according to claim 29, wherein said functional genomics is selected from the group consisting of mRNA profile analysis, protein expression profile analysis, polymerase chain reaction, Northern blot, Western blot, Nucleotide or amino acid sequence analysis, gene expression on a microarray, electrophoresis, 2-D electrophoresis, mass spectrometry, gas chromatography, liquid chromatography nuclear magnetic resonance, infrared, and atomic adsorption.
31. The method according to claim 1, wherein said analyzing of said cytoplasmic RNA for the presence of at least two genetic markers is accomplished by multigene RT-PCR.
32. The method according to claim 1, wherein said analyzing of said cytoplasmic RNA for said genetic markers comprises the further steps of:
    a. reverse transcripting said genetic markers with at least one set of gene specific primers all of which have a universal primer extension on the 5' terminus;
    b. removing said gene specific primers;
    c. amplifying a gene specific amplicon with said universal primer extensions in a PCR amplification; and
    d. identifying said gene specific amplicon.
33. The method according to claim 32, wherein said removing of said gene specific primers is accomplished using a method selected from the group consisting of molecular size exclusion, solid support selective attachment, and single strand specific DNase, and thereafter incorporating uracil-N-glycosylase with DNA oligonucleotide primers synthesized with deoxyUridine.

34. The method according to claim 32, wherein said removing of said gene specific primers is accomplished with uracil-N-glycosylase treatment of DNA oligonucleotide primers synthesized with deoxyUridine.
35. The method according to claim 34, wherein said uracil-N-glycosylase treatment is followed by incorporation of DNase-free RNases.
36. The method according to claim 33, wherein said gene specific primers are used under conditions of high primer-target annealing specificity.
37. The method according to claim 36, wherein said high primer-target annealing specificity is accomplished with proteins from natural recombination cellular repair mechanisms.
38. The method according to claim 37, wherein said high primer-target annealing specificity is accomplished with recA.
39. The method according to claim 32, wherein said identifying said gene specific amplicon is accomplished by its unique Rf value in size-based analysis systems.
40. The method according to claim 39, wherein said size-based analysis systems are selected from the group consisting of PAGE, agarose gel electrophoresis, capillary gel electrophoresis, SELDI, MALDI, and cDNA arrays.
41. The method according to claim 1, wherein said analyzing step further comprises:
    a. preamplifying said nucleic acids extracted by linear amplification wherein said preamplifying results in at least 1000 fold increase in all library transcripts in the from of aRNA;
    b. synthesizing a second strand from said aRNA only for up to 1000 independent selected genes of interest; and
    c. recognizing an amplified product using a method selected from the group consisting of array analysis, electrophoresis, and combinations thereof.
42. The method according to claim 41, wherein said preamplifying is accomplished by using a polymerase promoter selected from the group consisting of SP6 RNA polymerase promoter, T3 RNA polymerase promoter, and T7 RNA polymerase promoter.
43. The method according to claim 41, wherein said preamplifing is accomplished by using RNA polymerase using random primers.
44. The method according to claim 41, wherein said synthesizing of said second strand is under conditions of high primer-target annealing specificity.

45.The method according to claim 41, wherein said high primer-target annealing specificity is accomplished with proteins from natural recombination cellular repair mechanisms.

46.The method according to claim 41, wherein said high primer-target annealing specificity is accomplished with recA.

47.The method according to claim 41, wherein said recognizing is by pretreatment with DNase-free RNases.

48.The method according to claim 47, wherein said pretreatment is accomplished by performing a method selected from the group consisting of phenol extraction, silica binding, and combinations thereof.

49.The method according to claim 41, wherein said recognizing is accomplished by amplification of all double-stranded products.

50. The method according to claim 41, wherein said recognizing is accomplished by performing a method selected from the group consisting of array analysis, electrophoresis, and combinations thereof.

51.A method for improving signal-to-noise in the detection of distinct target sequences, which method comprises:

a. isolating nucleic acids;

b. preamplifying said nucleic acids by linear amplification wherein said preamplifying results in at least 1000 fold increase in all library transcripts in the from of aRNA;

c. synthesizing a second strand from said aRNA only for at least 2 independent selected genes of interest;

d. purifying double-stranded product; and

e. identifying said product.

52.The method according to claim 51, wherein said nucleic acids are selected from the group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.

53.The method according to claim 51, wherein said nucleic acids are cytoplasmic mRNA.

54.The method according to claim 51, wherein said isolating of said nucleic acids is accomplished by performing a method selected from the group consisting of RNA or

DNA chemical extractions, electrophoresis, chromatography, immunoseparations and affinity techniques.

55. The method according to claim 51, wherein said isolating of said nucleic acids is by capture with magnetic beads affixed to oligo(dT).

56. The method according to claim 51, wherein said preamplifying is by using a polymerase/promoter selected from the group consisting of SP6 RNA polymerase/promoter, T3 RNA polymerase/promoter, and T7 RNA polymerase/promoter.

57. The method according to claim 51, wherein said preamplifing is accomplished with RNA polymerase using random primers.

58. The method according to claim 51, wherein said synthesizing of said second strand is under conditions of high primer-target annealing specificity.

59. The method according to claim 58, wherein said high primer-target annealing specificity is accomplished with proteins from natural recombination cellular repair mechanisms.

60. The method according to claim 58, wherein said high primer-target annealing specificity is accomplished with recA.

61. The method according to claim 51, wherein said purifying said double-stranded products is accomplished with DNase-free RNases.

62. The method according to claim 51, wherein said purifying is accomplished by treatment from a group consisting of phenol extraction, silica binding, and combinations thereof.

63. The method according to claim 51, wherein said identifying is accomplished by amplification of said double stranded products.

64. The method according to claim 51, wherein said identifying step is accomplished by a method selected from the group consisting of array analysis, electrophoresis, and combinations thereof.

65. A method for acquiring intact cytoplasmic biomolecules from cells, which method comprises:

a. obtaining a fluid sample from a test subject, said fluid sample comprising a mixture of cell populations suspected of containing target cytoplasmic biomolecules;

b. fixing said cell populations;

c. recovering said cytoplasmic biomolecules; and

d. analyzing said cytoplasmic biomolecules.

66. The method according to claim 65, wherein said fixing is accomplished by treatment with a cell stabilizing agent.

67. The method according to claim 66, wherein said stabilizing agent is selected from the group consisting of aldehydes, urea, and combinations thereof.

68. The method according to claim 67, wherein said aldehyde is selected from the group consisting of formaldehyde, paraformaldehyde, and combinations thereof.

69. The method according to claim 68, wherein said stabilizing agent is a dialdehyde.

70. The method according to claim 69, wherein said dialdehyde is selected from the group consisting of glutaraldehyde, glyoxal, and combinations thereof.

71. The method according to claim 65, wherein said recovering of said cytoplasmic biomolecules is accomplished from macromolecular complexes formed after exposure to said stabilizing agent.

72. The method according to claim 71, wherein said recovering said cytoplasmic biomolecules from said cells is accomplished by enzymatic digestion.

73. The method according to claim 72, wherein said enzymatic digestion is accomplished by using a member selected from the group consisting of proteinases, nucleophiles, and combinations thereof.

74. The method according to claim 73, wherein said nucleophiles are selected from the group consisting of phosphate-based buffers, tris-based buffers, acetic hydrazide, hydroxylamine, and combinations thereof.

75. The method according to claim 73, wherein said proteinases are selected from the group consisting of proteinase K digestion, V8 proteinase digestion, pronase digestion, and combinations thereof.

76. The method according to claim 65, wherein said cytoplasmic biomolecules are proteins.

77. The method according to claim 76, wherein said recovering of said proteins is accomplished by a method selected from the group consisting of chemical extractions, electrophoresis, chromatography, immunoseparations and affinity techniques.

78. The method according to claim 65, wherein said cytoplasmic biomolecules are nucleic acids.

79. The method according to claim 78, wherein said nucleic acids are selected from the group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.
80. The method according to claim 78, wherein said nucleic acids are cytoplasmic mRNA.
81. The method according to claim 78, wherein said analyzing of said nucleic acids is accomplished by a method selected from the group consisting of RNA or DNA chemical extractions, electrophoresis, chromatography, immunoseparations and affinity techniques.
82. The method according to claim 78, wherein said analyzing of said nucleic acids is accomplished by capture with magnetic beads affixed to oligo(dT).
83. A method for amplifying multiple genetic markers in the same reaction mix, which method comprises:
    a. reverse transcripting said genetic markers with at least one set of gene specific primers all of which have a universal primer extension on the 5' terminus;
    b. removing said gene specific primers;
    c. amplifying a gene specific amplicon with said universal primer extensions in a PCR amplification; and
    d. identifying said gene specific amplicon.
84. The method according to claim 83, wherein said removing of said gene specific primers is accomplished by a method selected from the group consisting of molecular size exclusion, solid support selective attachment, single strand specific DNase, and incorporating uracil-N-glycosylase with DNA oligonucleotide primers synthesized with deoxyUridine.
85. The method according to claim 83, wherein said removing of said gene specific primers is accomplished with uracil-N-glycosylase treatment of DNA oligonucleotide primers synthesized with deoxyUridine.
86. The method according to claim 85, wherein said uracil-N-glycosylase treatment is followed by incorporation of DNase-free RNases.
87. The method according to claim 83, wherein said gene specific primers are used under conditions of high primer-target annealing specificity.
88. The method according to claim 87, wherein said high primer-target annealing specificity is accomplished with proteins from natural recombination cellular repair mechanisms.

89. The method according to claim 88, wherein said high primer-target annealing specificity is accomplished with recA.

90. The method according to claim 83, wherein said identifying said gene specific amplicon is accomplished by its unique Rf value in size-based analysis systems.

91. The method according to claim 90, wherein said size-based analysis systems are selected from the group consisting of PAGE, agarose gel electrophoresis, capillary gel electrophoresis, SELDI, MALDI, and cDNA arrays.

92. Apparatus for extracting intact cytoplasmic biomolecules from cells, comprising:

    a. means for obtaining a fluid sample from a test subject, said fluid sample comprising a mixture of cell populations suspected of containing target cells;

    a. means for releasing said cytoplasmic biomolecules from said cells;

    b. means for isolating said cytoplasmic biomolecules; and

    c. means for analyzing said cytoplasmic biomolecules.

93. Apparatus as claimed in claim 92, wherein said fluid sample is whole blood.

94. Apparatus as claimed in claim 92, wherein said means for obtaining said fluid sample is by a group consisting of immunomagnetic selection means, cell fractionation means, and combination means thereof.

95. Apparatus according to claim 92, wherein said means for releasing is by permeabilizing agent addition.

96. Apparatus according to claim 97, wherein said permeabilizing agent is from a group consisting of a detergent, surfactant, and combinations thereof.

97. Apparatus according to claim 95, wherein said permeabilizing agent is from a group consisting of saponin, Immuniperm, and combinations thereof.

98. Apparatus according to claim 95, wherein said permeabilizing agent is Immuniperm.

99. Apparatus according to claim 92, wherein means for obtaining said fluid sample is by means for treatment with cell stabilizing agent.

100. Apparatus according to claim 99, wherein said stabilizing agent is from a group consisting of aldehydes, urea, and combinations thereof.

101. Apparatus according to claim 100, wherein said aldehyde is from a group consisting of formaldehyde, paraformaldehyde, and combinations thereof.

102. Apparatus according to claim 100, wherein said stabilizing agent is a dialdehyde.

103. Apparatus according to claim 102, wherein said dialdehyde is from a group consisting of glutaraldehyde, glyoxal, and combinations thereof.

104. Apparatus according to claim 99, wherein said means for releasing of said cytoplasmic biomolecules are from macromolecular complexes formed after exposure to said stabilizing agent.

105. Apparatus according to claim 99, wherein said means for releasing said cytoplasmic biomolecules from said cells through enzymatic digestion means.

106. Apparatus according to claim 105, wherein said means for enzymatic digestion occurs through a group consisting of proteinase means, nucleophile means, and combination means thereof.

107. Apparatus according to claim 106, wherein said nucleophile means is from a group consisting of phosphate-based buffer means, tris-based buffer means, acetic hydrazide means, hydroxylamine means, and combination means thereof.

108. Apparatus according to claim 106, wherein said proteinase means is from a group consisting of proteinase K digestion means, V8 proteinase digestion means, pronase digestion means, and combination means thereof.

109. Apparatus according to claim 92, wherein said cytoplasmic biomolecules are proteins.

110. Apparatus according to claim 109, wherein said means for isolating said proteins is from a group consisting of chemical extractions means, electrophoresis means, chromatography means, immunoseparation means and affinity techniques means.

111. Apparatus according to claim 92, wherein said cytoplasmic biomolecules are nucleic acids.

112. Apparatus according to claim 114, wherein said nucleic acids are from a group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.

113. Apparatus according to claim 111, wherein said nucleic acids are cytoplasmic mRNA.

114. Apparatus according to claim 111, wherein said means for isolating of said nucleic acids is from a group consisting of RNA or DNA chemical extractions means, electrophoresis means, chromatography means, immunoseparation means and affinity techniques means.

115. Apparatus according to claim 113, wherein said means for said isolating is by capturing means with magnetic beads affixed to oligo(dT).

116. Apparatus according to claim 92, wherein means for assessing target cell phenotypic expression other than with said cytoplasmic biomolecules.

117. Apparatus according to claim 116, wherein said means of phenotypic expression is from a group consisting of morphological examinating means, cell component staining means, immunoanalyzing means, and combination means thereof.

118. Apparatus according to claim 92, wherein said means for analyzing said cytoplasmic biomolecules is by functional proteomics means.

119. Apparatus according to claim 118, wherein said means for functional proteomics is from a group consisting of protein expression profile means, Western blot means, amino acid sequence analysis means, electrophoresis means, 2-D electrophoresis means, mass spectrometry means, gas chromatography means, liquid chromatography means, nuclear magnetic resonance means, infrared means, atomic adsorption means, and combination means thereof.

120. Apparatus according to claim 92, wherein said means for analyzing said cytoplasmic biomolecules is by functional genomics means.

121. Apparatus according to claim 120, wherein said functional genomics means is from a group consisting of mRNA profile analysis means, protein expression profile analysis means, polymerase chain reaction means, Northern blot means, Western blot means, Nucleotide or amino acid sequence analysis means, means of gene expression on a microarray, electrophoresis means, 2-D electrophoresis means, mass spectrometry means, gas chromatography means, liquid chromatography means, nuclear magnetic resonance means, infrared means, and atomic adsorption means.

122. Apparatus according to claim 92, wherein said means for analyzing said cytoplasmic RNA for the presence of at least two genetic markers is by multigene RT-PCR means.

123. Apparatus according to claim 92, wherein said means for analyzing said cytoplasmic RNA for said genetic markers comprises:

a. means for reverse transcripting said genetic markers with at least one set of gene specific primers all of which have a universal primer extension on the 5' terminus;

b. means for removing said gene specific primers;

c. means for amplifying a gene specific amplicon with said universal primer extensions in a PCR amplification; and

d. means for identifying said gene specific amplicon.

124. Apparatus according to claim 123, wherein said means for removing of said gene specific primers is from a group consisting of molecular size exclusion means, solid support selective attachment means, single strand specific DNase means, and means for incorporating uracil-N-glycosylase with DNA oligonucleotide primers synthesized with deoxyUridine.

125. Apparatus according to claim 123, wherein said means for removing of said gene specific primers is by means for uracil-N-glycosylase treatment of DNA oligonucleotide primers synthesized with deoxyUridine.

126. Apparatus according to claim 123, wherein said means for removing said gene specific primers is by means for incorporation of DNase-free RNases.

127. Apparatus according to claim 123, wherein said gene specific primers are used with means for conditions of high primer-target annealing specificity.

128. Apparatus according to claim 127, wherein said means for high primer-target annealing specificity is with proteins from natural recombination cellular repair mechanisms.

129. Apparatus according to claim 128, wherein said means for high primer-target annealing specificity is with recA.

130. Apparatus according to claim 123, wherein said means for identifying said gene specific amplicon is by means using unique Rf value in size-based analysis systems.

131. Apparatus according to claim 130, wherein said means for size-based analysis systems is from a group consisting of PAGE means, agarose gel electrophoresis means, capillary gel electrophoresis means, SELDI means, MALDI means, and means for cDNA arrays.

132. Apparatus according to claim 92, wherein said analyzing means comprises:

a. means for preamplifying said nucleic acids extracted by linear amplification means wherein said preamplifying means results in at least 1000 fold increase in all library transcripts in the from of aRNA;

b. means for synthesizing a second strand from said aRNA only for up to 1000 independent selected genes of interest; and

c. means for recognizing an amplified product from a group consisting of array analysis means, electrophoresis means, and combination means thereof.

133. Apparatus according to claim 132, wherein said means for preamplifying is from a group consisting of SP6 RNA polymerase promoter means, T3 RNA polymerase promoter means, and T7 RNA polymerase promoter means.

134. Apparatus according to claim 132, wherein said means for preamplifing is with RNA polymerase means using random primers.

135. Apparatus for improving signal-to-noise in the detection of distinct target sequences comprising:

a. means for isolating nucleic acids;

b. means for preamplifying said nucleic acids by linear amplification means wherein said means for preamplifying results in at least 1000 fold increase in all library transcripts in the from of aRNA;

c. means for synthesizing a second strand from said aRNA only for at least 2 independent selected genes of interest;

d. means for purifying double-stranded product; and

e. means for identifying said product.

136. Apparatus according to claim 135, wherein said nucleic acids are from a group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.

137. Apparatus according to claim 135, wherein said nucleic acids are cytoplasmic mRNA.

138. Apparatus according to claim 135, wherein said means for isolating of said nucleic acids is from a group consisting of RNA or DNA chemical extractions means, electrophoresis means, chromatography means, immunoseparation means and affinity techniques means.

139. Apparatus according to claim 135, wherein said means for isolating of said nucleic acids is by capturing means with magnetic beads affixed to oligo(dT).

140. Apparatus according to claim 135, wherein said means for preamplifying is from a group consisting of SP6 RNA polymerase/promoter means, T3 RNA polymerase/promoter means, and T7 RNA polymerase/promoter means.

141. Apparatus according to claim 135, wherein said means for preamplifing is by RNA polymerase means using random primers.

142.Apparatus according to claim 135, wherein said means for synthesizing of said second strand is by means for conditions of high primer-target annealing specificity.

143.Apparatus according to claim 142, wherein said means for high primer-target annealing specificity is with proteins from natural recombination cellular repair mechanisms.

144.Apparatus according to claim 143, wherein said means for high primer-target annealing specificity is with recA.

148.Apparatus according to claim 138, wherein said means for purifying of said double stranded products is with DNase-free Rnases means.

148.Apparatus according to claim 135, wherein said means for purifying is from a group consisting of phenol extraction means, silica binding means, and combination means thereof.

149.Apparatus according to claim 135, wherein said means for identifying is by amplification means for said double stranded products.

150.Apparatus according to claim 149, wherein said means for identifying is by said amplification means from a group consisting of array analysis means, electrophoresis means, and combination means thereof.

151. Apparatus for acquiring intact cytoplasmic biomolecules from cells, comprising:

a. means for obtaining a fluid sample from a test subject, said fluid sample comprising a mixture of cell populations suspected of containing target cytoplasmic biomolecules;

d. means for fixing said cell populations;

e. means for recovering said cytoplasmic biomolecules; and

f. means for analyzing said cytoplasmic biomolecules.

152. Apparatus according to claim 151, wherein said means for fixing is by treatment means with a cell stabilizing agent.

153. Apparatus according to claim 152, wherein said stabilizing agent is from a group consisting of aldehydes, urea, and combinations thereof.

154. Apparatus according to claim 153, wherein said aldehyde is from a group consisting of formaldehyde, paraformaldehyde, and combinations thereof.

155. Apparatus according to claim 152, wherein said stabilizing agent is a dialdehyde.

156. Apparatus according to claim 155, wherein said dialdehyde is from a group consisting of glutaraldehyde, glyoxal, and combinations thereof.

157. Apparatus according to claim 152, wherein said means for recovering of said cytoplasmic biomolecules are from macromolecular complexes formed after exposure to said stabilizing agent.

158. Apparatus according to claim 152, wherein said means for recovering said cytoplasmic biomolecules from said cells is by enzymatic digestion means.

160. Apparatus according to claim 158, wherein said enzymatic digestion means is through a group consisting of proteinase means, nucleophile means, and combination means thereof.

161. Apparatus according to claim 160, wherein said nucleophile means is from a group consisting of phosphate-based buffer means, tris-based buffer means, acetic hydrazide means, hydroxylamine means, and combination means thereof.

162. Apparatus according to claim 160, wherein said proteinase means is from a group consisting of proteinase K digestion, V8 proteinase digestion, pronase digestion, and combinations thereof.

163.Apparatus according to claim 151, wherein said cytoplasmic biomolecules are proteins.

164. Apparatus according to claim 151, wherein said means for recovering said proteins is from a group consisting of chemical extraction means, electrophoresis means, chromatography means, immunoseparation means and affinity techniques means.

165. Apparatus according to claim 151, wherein said cytoplasmic biomolecules are nucleic acids.

166. Apparatus according to claim 165, wherein said nucleic acids are from a group consisting of cytoplasmic RNA, nuclear and mitochondrial RNA, nuclear and mitochondrial DNA, and combinations thereof.

167. Apparatus according to claim 165, wherein said nucleic acids are cytoplasmic mRNA.

168. Apparatus according to claim 165, wherein said means for analyzing of said nucleic acids is from a group consisting of RNA or DNA chemical extraction means, electrophoresis means, chromatography means, immunoseparation means and affinity techniques means.

169. The method according to claim 165, wherein said means for analyzing of said nucleic acids are by capture means with magnetic beads affixed to oligo(dT).

170. A cell preparation kit for maintaining phenotypic and genotypic integrity of a single cell or population of cells comprising:

    a. target cell permeabilizing agents;
    b. target cell stabilizing agents;
    c. nucleic acid releasing agents; and
    d. a protocol for using the method of claim 66.

171. The kit as claimed in claim 170, wherein said kit further containing immunomagnetic particles having binding specificity for said target cells.

172. The kit as claimed in claim 170, wherein said permeabilizing agent is selected from the group consisting of saponin, detergents, surfactants and combinations thereof.

173. The kit as claimed in claim 170, wherein said permeabilizing agent is Immuniperm.

174. The kit as claimed in claim 170, wherein said stabilizing agent is selected from the group consisting of aldehydes, dialdehydes, urea and combinations thereof.

175. The kit as claimed in claim 170, wherein said releasing agent is selected from the group consisting of proteinases, nucleophiles, and combinations thereof.

176. The kit as claimed in claim 175, wherein said proteinase is selected from the group consisting of proteinase K, V8 proteinase, pronase, and combinations thereof.

177. The kit as claimed in claim 175, wherein said nucleophile is selected from the group consisting of phosphate-based buffers, tris-based buffers, acetic hydrazide, hydroxylamine, and combinations thereof.

178. A nucleotide amplification kit for increasing the signal-to-noise ratio in distinct target sequences comprising:

    a. nucleic acid isolating agents;
    b. preamplifying agents wherein said preamplifying agents generate an aRNA library with at least a 1000 fold increase in all transcripts;
    c. second strand synthesizing agents wherein said synthesizing agents target at least 2 independent selected transcripts of interest;
    d. purifying agents wherein said purifying agents select for double-stranded products;

e. nucleotide specific detecting agents wherein said detecting agents enable confirmation of double-stranded products; and

f. a protocol for using the method of claim 52.

179. The kit as claimed in claim 178, wherein said isolating agents are immunomagnetic particles having binding specificity for said nucleic acids.

180. The kit as claimed in claim 178, wherein said isolating agents are from a group consisting of RNA or DNA chemical extracting agents, electrophoresis agents, chromatography agents, immunoseparation agents and nucleotide affinity agents.

181. The kit as claimed in claim 178, wherein said preamplifying agents are from a group consisting of SP6 RNA polymerase/promoter, T3 RNA polymerase/promoter, and T7 RNA polymerase/promoter.

182. The kit as claimed in claim 178, wherein said preamplifying agent is RNA polymerase/random primers.

183. The kit as claimed in claim 178, wherein said second strand synthesizing agents are polymerase/primers with high primer-target annealing specificity.

184. The kit as claimed in claim 178, wherein said purifying agents are DNase-free Rnases.

185. The kit as claimed in claim 178, wherein said purifying agents are from a group consisting of phenol extraction agents and silica binding agents.

186. The kit as claimed in claim 178, wherein said nucleotide specific detecting agents is from a group consisting of double-stranded nucleotide amplification agents, array detection agents, and electrophoresis agents.